Figure S1. Gene-finding and functional annotation pipeline of whole genome assembles used in EzBioCloud genome database. Protein-coding sequences (CDSs) were predicted by Prodigal 2.6.2 (Hyatt *et al.*, 2010). Genes coding for tRNA were searched using tRNAscan-SE 1.3.1 (Schattner *et al.*, 2005). The rRNA and other non-coding RNAs were searched by a covariance model search with Rfam 12.0 database (Nawrocki & Eddy, 2013). CRISPRs were detected by PilerCR 1.06 (Edgar, 2007) and CRT 1.2 (Bland *et al.*, 2007). The CDSs were classified into groups based on their roles, with reference to orthologous groups (EggNOG 4.5; http://eggnogdb.embl.de) (Powell *et al.*, 2014). For more functional annotation, the predicted CDSs were compared with Swissprot (UniProt, 2015), KEGG (Kanehisa *et al.*, 2014) and SEED (Overbeek *et al.*, 2005) databases using UBLAST program (Edgar, 2010).

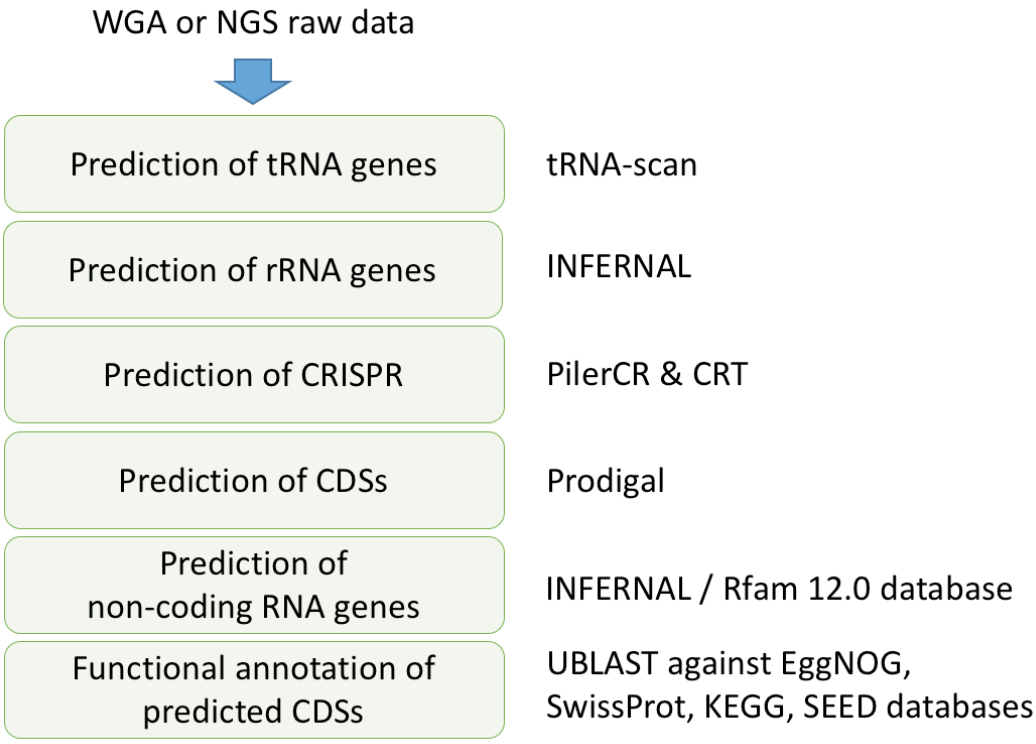


Figure S2. Bioinformatics pipeline for bacterial community analysis. The primer sequences were discarded using in-house JAVA program. Non-specific amplicons that do not encode 16S rRNA are detected by HMMER's hmmsearch program (Eddy, 2011) with 16S rRNA profiles. All sequences were denoised by DUDE-Seq (http://data.snu.ac.kr/pub/dude-seq/) and non-redundant reads were extracted by UCLUST-clustering (Edgar, 2010). Taxonomic identification was assigned against the EzBioCloud database using USEARCH (8.1.1861_i86linux32) (Edgar, 2010) followed by more precise pairwise alignment (Myers & Miller, 1988). The chimera sequences were detected by UCHIME (Edgar *et al.*, 2011). Only sequencing reads with lower than 97% similarity to EzBioCloud database were considered for chimera detection. Operational taxonomic units (OTUs) in the sample were investigated using open-reference method (Rideout *et al.*, 2014) with CD-HIT (Fu *et al.*, 2012) and UCLUST (Edgar, 2010). The alpha diversity indices and rarefaction curves were estimated by in-house code.

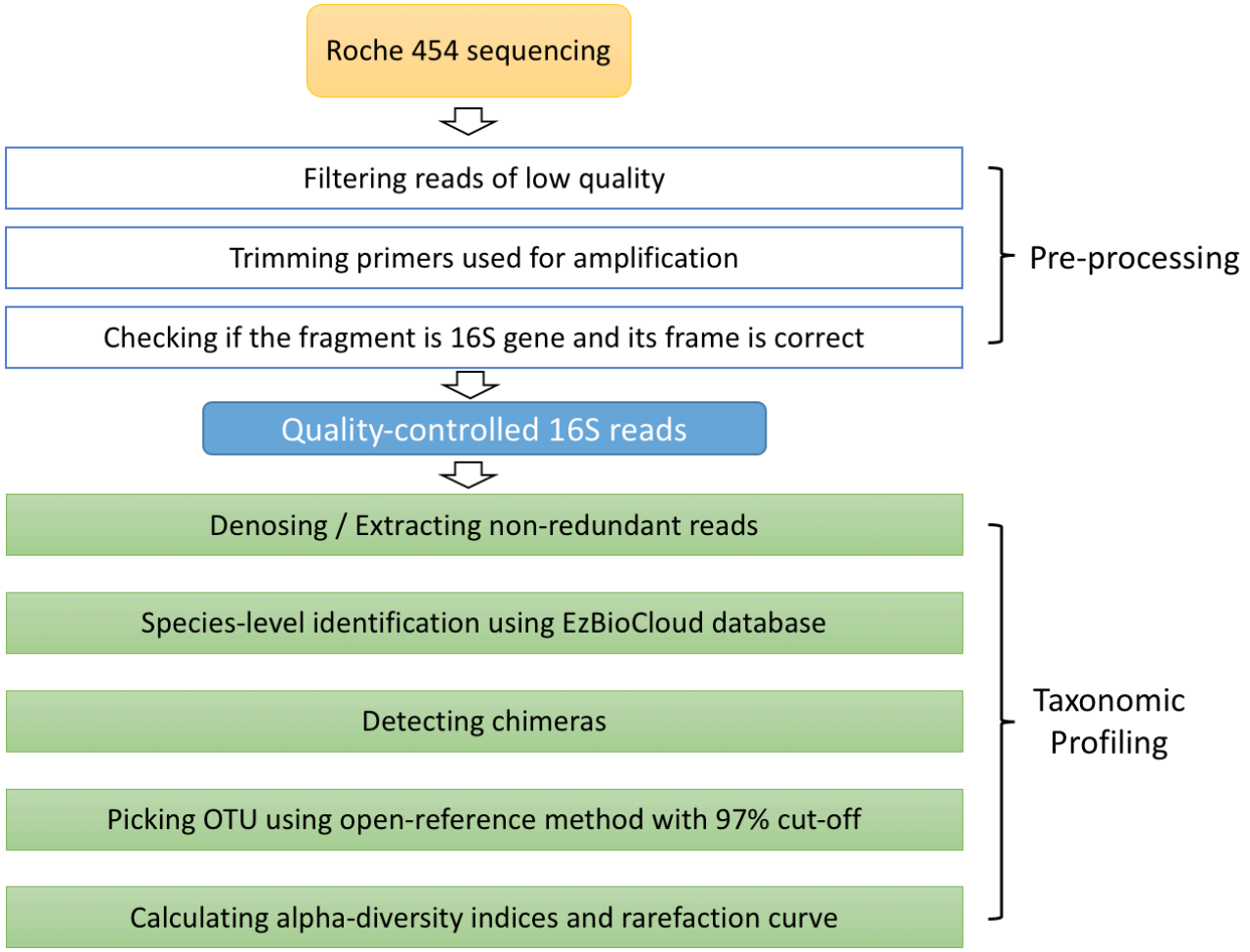
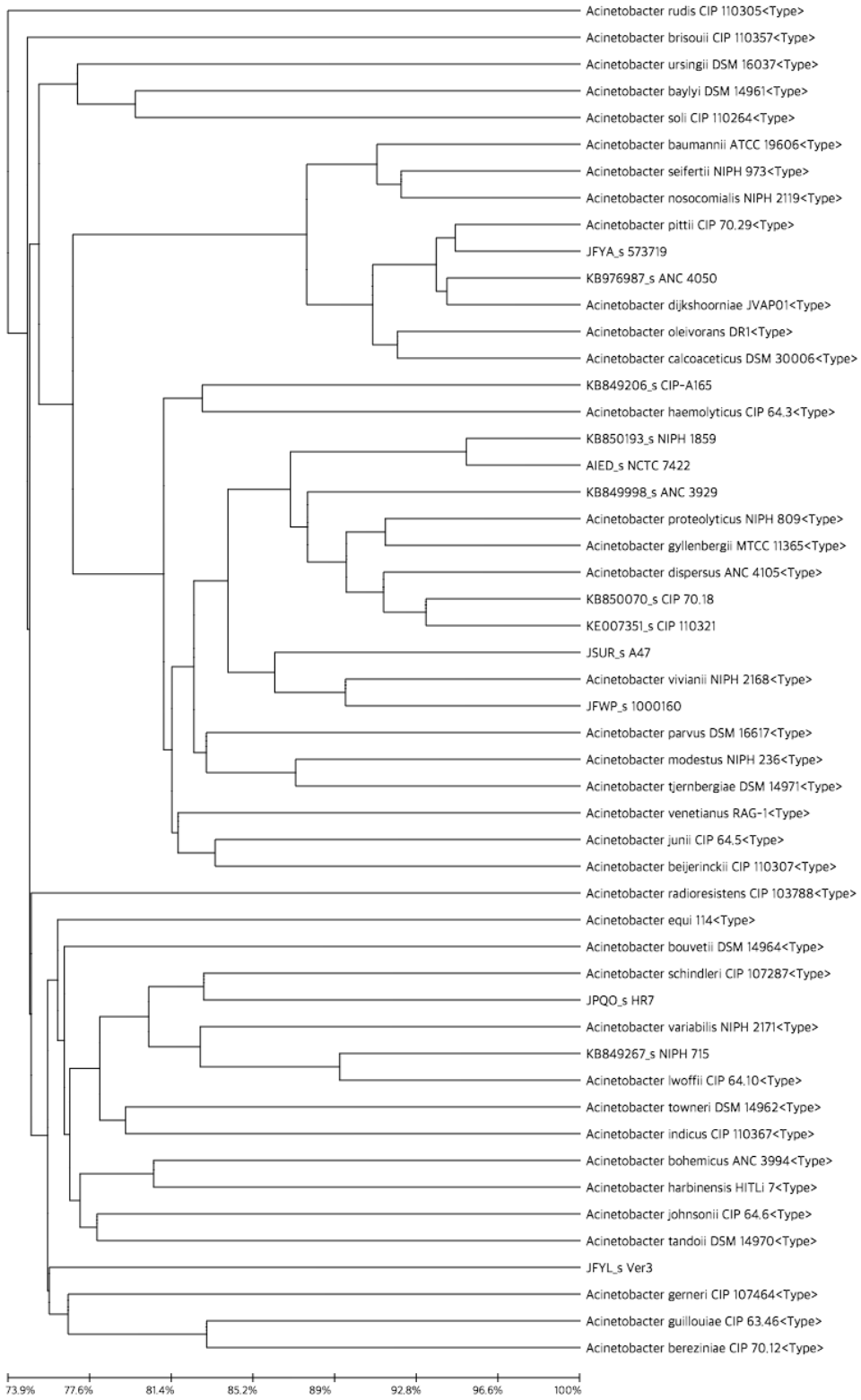


Figure S3. OrthoANI-based dendrogram of the genus *Acinetobacter* including 13 tentatively named species. The dendrogram is constructed using UPGMA algorithm. The scale bar represents OrthoANI values. <Type>, type strain.



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